

10 30 50
AAAGCACAGACTTCAGGTCTCCAAGGAGGATGGGTGGCTGCAGCACAAAGAGGCAAGCGGC
M G G C S T R G K R P

70 90 110
CGTCAGCCCTCAGTCTGCTGCTGCTGCTGCTGCTCGGGGATCGCAGCCCTCTGCCCTCC
S A L S L L L L L L L S G I A A S A L P
↑

130 150 170
CCCTGGAGAGCGGTCCCACCGGCCAGGACAGTGTGCAGGATGCCACAGGCGGGAGGAGGA
L E S G P T G Q D S V Q D A T G G R R T

190 210 230
CCGGCCTTCTGACTTTCCTTGCTGGTGGCATGAGTGGGCTTCCCAAGACAGCTCCAGCA
G L L T F L A W W H E W A S Q D S S S T

250 270 290
CCGCTTTCGAAGGGGTACCCCGGAGCTGTCTAAGCGGCAGGAAAGACCACCCCTCCAGC
A F E G G T P E L S K R Q E R P P L Q Q

310 330 350
AGCCCCACACCGGGGATAAAAAGCCCTGCAAGAACTTCTTCTGGAAAACCTTCTCCTCGT
P P H R D K K P C K N F F W K T F S S C

370 390 410
GCAAGTAGCCCGAGCCTGACCGGAGCCTGACCGGCCACCCTGTGAATGCAGCCGTGGCCT
K

430
GAATAAAGAGTGTCAAGT

```

CST      10 RPSALSLLLLLLLLSGIAASALPLESGPTGQDSVQDATGGRTGLLTFLAW 59
          ... .| ::| |:|:..: . . |.:..||| . : . : :
SST      7 QCALAALCIVLALGGVTGAPSDPRLRQFLQKSLAAATGQELAKYFLAEL 56

          ↓                               ↓
CST      60 WHEWASQDSSSTAFEGGTPELSRQERPPPLQQ.....PPHRLKPCCK 101
          : | . :... . |: ... : | .|| . :|: | .||
SST      57 LSEFNQTENDALEPEDLPQAAEQDEMRLELQPSANSNPAMAPRKAAGCK 106

          ↑                               ↑

CST      102 NFEWKTFFSSCK
          |||||..||
SST      107 NFEWKTFTSC

```

FIGURE 2

GCACGAGGCT CAGCAGGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC	51
Met Met Gly Gly Arg Gly Thr Gly Gly	
1 5	
AAG TGG CCC TCA GCC TTC GGG <u>CTG CTG CTG</u> CTC TGG GGG GTC GCA GCC	99
Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala	
10 15 20 25 ↑	
TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG	147
Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln	
30 35 40	
GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG	195
Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp	
45 50 55	
CAC GAG TCG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT	243
His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly	
60 65 70	
ACC CCC GGG CTG TCC AAG AGC <u>CAG GAA AGG CCA CCC CCC CAA CAG CCC</u>	291
Thr Pro Gly Leu Ser Lys Ser <u>Gln Glu Arg Pro Pro Pro Gln Gln Pro</u>	
75 80 85	
<u>CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC</u>	339
<u>Pro His Leu Asp</u> Lys Lys <u>Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe</u>	
90 95 100 105	
TCC TCG TGC AAG TAA CCC CAC CCT GGG CAT AGC ACC CTG GCC ACC CTG	387
Ser Ser Cys Lys * 110 115 120	
TGA GAT GCC AAC GAG ACC TGA ATA AAG ACT GTC AAT CAA C	427
125 130	

FIGURE 3

MOUSE CSTGCACGAG	GCTCAGCAG	TCCGAGGATG	ATGGGTGGCC
RAT CTAAAGCACAG	ACTTCAGGTC	TCCAAGGAGG	ATGGGTGGCT
HUMAN CST	GGCACGAGGC	CAAACATTGA	TTTCAGGGCT	GCCAGGAGG	AAGAGCAGCA
MOUSE CST	GAGGCACAGG	AGGCAAGTGG	CCCTCAG...CCTTC
RAT CST	GCAGCACAAG	AGGCAAGCGG	CCGTCAG...CCCTC
HUMAN CST	GCAGGGTGGG	AGAGAAGCTC	CAGTCAGCCC	ACAAGATGCC	ATTGTCCCCC
MOUSE CST	GG.....	.GCTGCTGCT	GCTCTGGGGG	GTCGCAGCCT	CGGCCCTTCC
RAT CST	<u>AGTCTGCTGC</u>	<u>TGCTGCTGCT</u>	GCTCTCGGGG	ATCGCAGCCT	CTGCCCTCCC
HUMAN CST	<u>GGCCTCCTGC</u>	<u>TGCTGCTGCT</u>	CTCCGGGGCC	ACGGCCACCG	CTGCCCTGCC
MOUSE CST	CCTGGAGAGT	GGCCCTACTG	GCCAGGACAGTGTG	CAGGAAGCCA
RAT CST	CCTGGAGAGC	GGTCCCACCG	GCCAGGACAGTGTG	CAGGATGCCA
HUMAN CST	CCTGGAGGGT	GGCCCCACCG	GCCGAGACAG	CGAGCATATG	CAGGAAGCGG
MOUSE CST	C...CGAGGG	GAGGAGCGGC	CTTCTGACTT	TCCTTGCCCTG	GTGGCAGCAG
RAT CST	CAGGCGGGAG	GAGGACCGGC	CTTCTGACTT	TCCTTGCCCTG	GTGGCATGAG
HUMAN CST	CAGGAATAAG	GAAAAGCAGC	CTCCTGACTT	TCCTCGCTTG	GTGGTTTGAG
MOUSE CST	TGGGCTTCCC	AAGCCAGCTC	CAGCACCCCC	GTCGGAGGGG	GTACCCCCGG
RAT CST	TGGGCTTCCC	AAGACAGCTC	CAGCACCGCT	TTCGAAGGGG	GTACCCCCGA
HUMAN CST	TGGACCTCCC	AGGCCAGTGC	CGGGCCCCCTC	ATAGGAGAGG	AAGCCCCGGA
MOUSE CST	GCTGTCCAAG	AGCCAGGAAA	GGCCACCCCC	CCAACA3CCC	CCACACCTGG
RAT CST	GCTGTCTAAG	CGGCAGGAAA	GACCACCCCT	CCAGCA3CCC	CCACACCGGG
HUMAN CST	GGTGGCCAGG	CGGCAGGAAG	GCGCACCCCC	CCAGCATCC	GCGCGCCGGG
MOUSE CST	ATAAAAAGCC	CTGCAAGAAC	TTCTTCTGGA	AAACCTTCTC	CTCGTGCAAG
RAT CST	ATAAAAAGCC	CTGCAAGAAC	TTCTTCTGGA	AAACCTTCTC	CTCGTGCAAG
HUMAN CST	ACAGAAATGCC	CTGCAGGAAC	TTCTTCTGGA	AGACCTTCTC	CTCCTGCAAA
MOUSE CST	TAACCCACCC	CTGGGCATAG	CACCCTGGCC	ACCCTGTGAG	ATGCCAACGA
RAT CST	TAGCCCGAGC	CTGACCGGAG	CCTGACCGGC	CACCCTGTGA	ATGCAGCCGT
HUMAN CST	TAAACCTCA	CCCATGAATG	C.....	.TCACGCAAG	TGTAATGACA
MOUSE CST	GACCTGAATA	AAGACTGTCA	ATCAAC....
RAT CST	GGCCTGAATA	AAGAGTGTCA	AGT.....
HUMAN CST	GACCTGAATA	AAATGTATTA	AGCAGCAGTG	ATCTTTCCCTC	TCCTCCTTCC
		*			
MOUSE CST
RAT CST
HUMAN CST	CAAGTCATTG	AAAAGTGTTT	GTTATTTAAA	TTCCATAAT	GCCCAATACT
MOUSE CST
RAT CST
HUMAN CST	GACGTGTCTT	GAGTAATTTG	GAACCCAAAA	GTGAAGATCT	TTGATAAAGA
MOUSE CST
RAT CST
HUMAN CST	TTTTTTTTTGT	GGTTCGACTG	GACTGTGCTG	AGTGCGGGCA	CTGGGCTTTT
MOUSE CST
RAT CST
HUMAN CST	CTTCTGATGT	TCATTATGGT	GCTGGGAAGC	TCTGTCTTTG	ATTTAAATA
					*
MOUSE CST
RAT CST
HUMAN CST	AAATAGCTAA	AGGCTACAC

FIGURE 3a

	1					50
RAT CST	.MGGCSTRGK	RPSALSLLLL	LLLSGIAASA	LPLESGPTGQ	DS..VQDATG	
MOUSE CST	MMGGRGTGGK	WPSAFGLLLL	W...GVAASA	LPLESGPTGQ	DS..VQEATE	
HUMAN CST	MPLSPGLLLL	LLSGATATAA	LPLEGGPTGR	DSEHMQEAAG	
Consensus	-----	-P-----	LLLL	-----A--A	LPLE-GPTG-	DS---Q-A--
	51					100
RAT CST	GRRTGLLTFL	AWWHEWASQD	SSSTAFEGGT	PELSKRQERP	PLQQPPHRDK	
MOUSE CST	G.RSGLLTFL	AWWHEWASQA	SSSTPVGGGT	PGLSKSQERP	PPQQPPHLDK	
HUMAN CST	IRKSSLLTFL	AWWFEWTSQA	SAGPLIGEEA	REVARRQEGA	PPQQSARRDR	
Consensus	-----	LLTFL	AWW-EW-SQ-	S-----	-----QE--	P-QQ-----D-
	101		116			
RAT CST	KPCKNFFWKT	FSSCK				
MOUSE CST	KPCKNFFWKT	FSSCK				
HUMAN CST	MPCRNFFWKT	FSSCK				
Consensus	-PC-NFFWKT	FSSCK				

FIGURE 3b

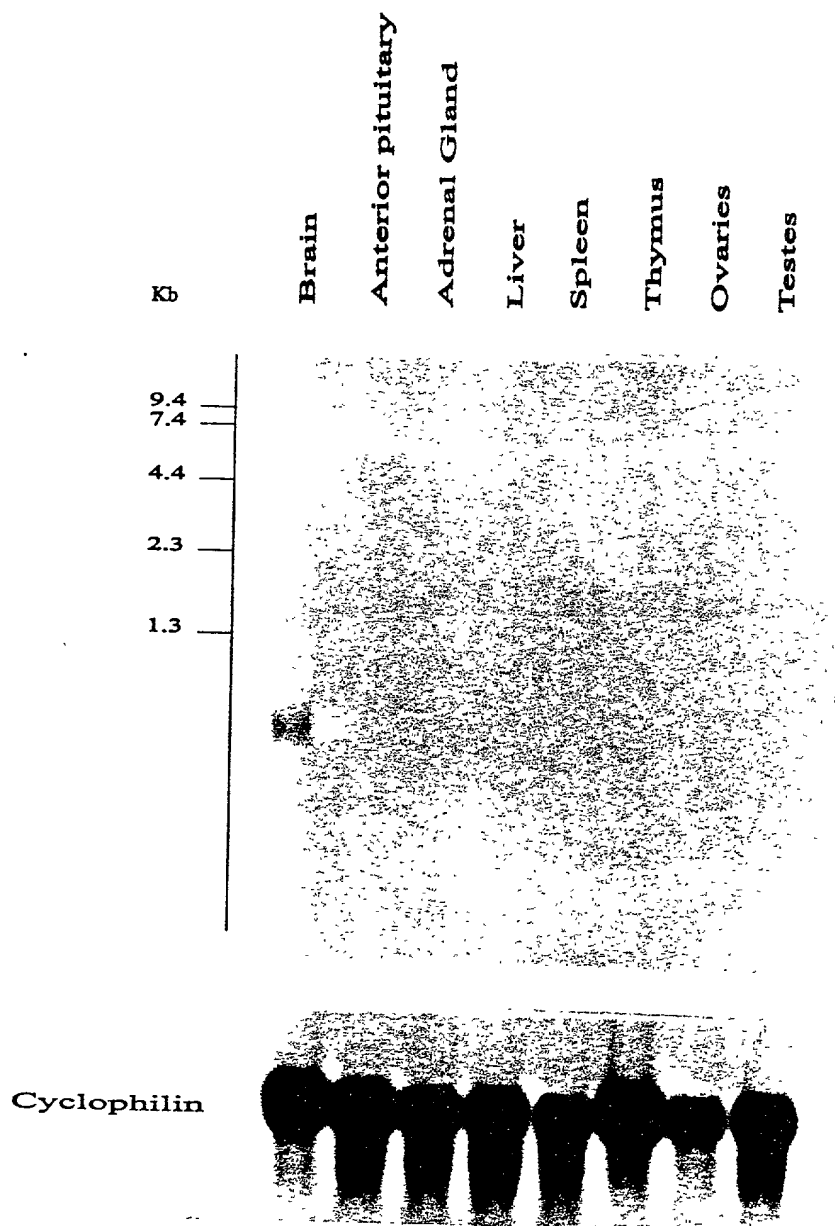
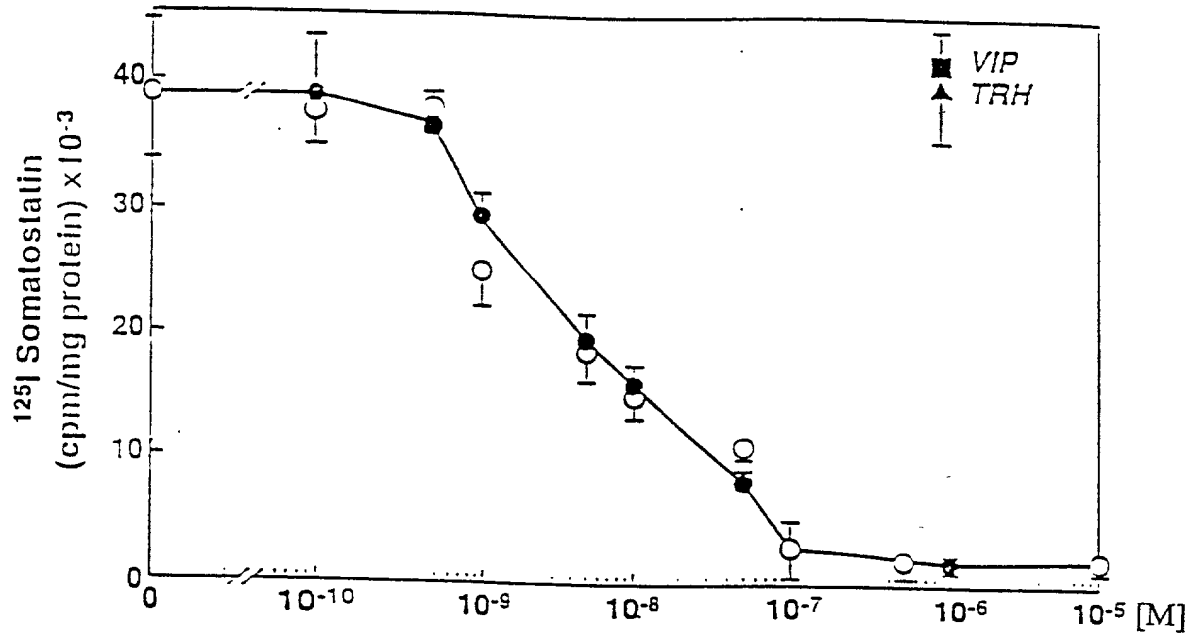
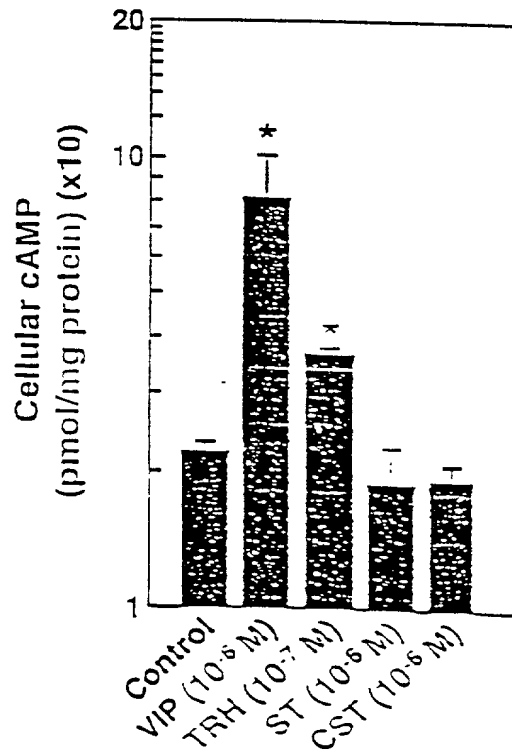


FIGURE 4

5A



5B



5C

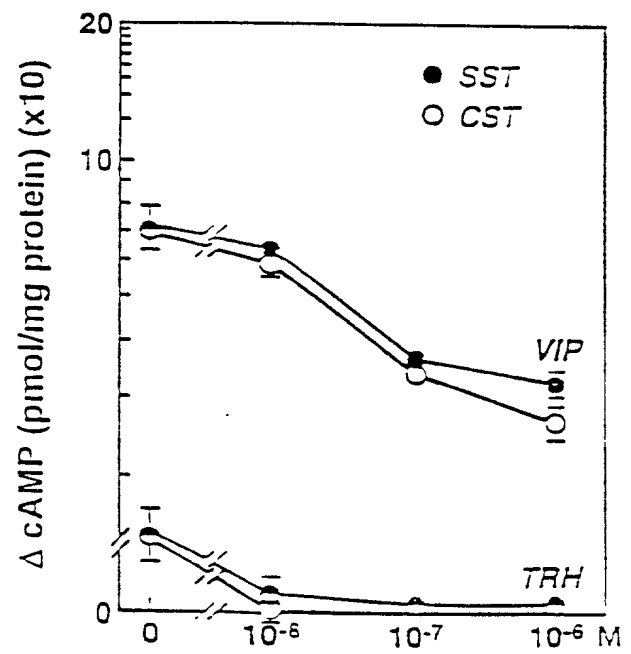
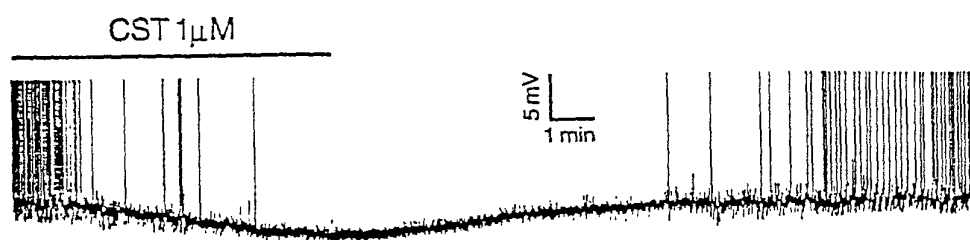
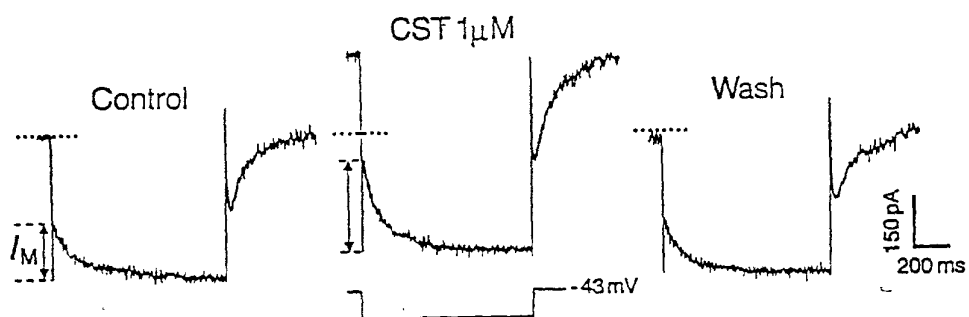


FIGURE 5

6A



6B



6C

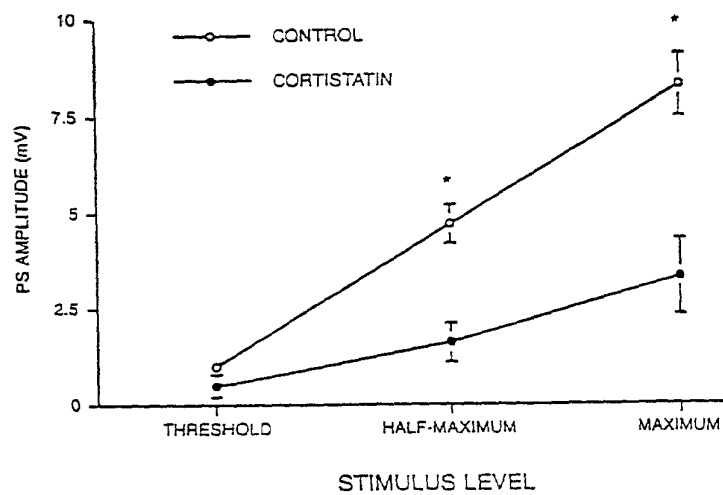
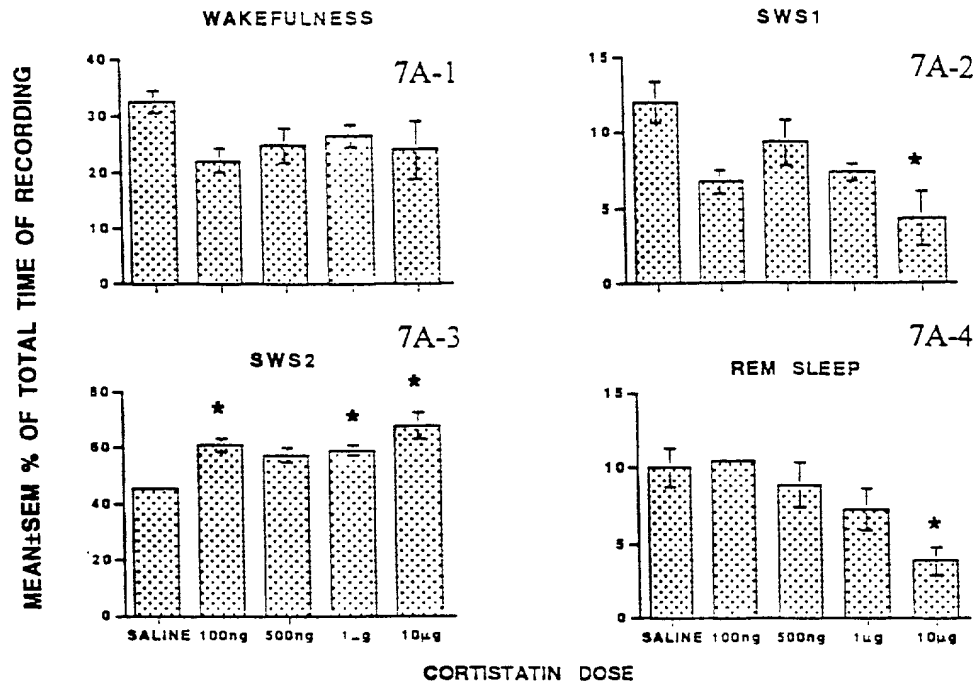
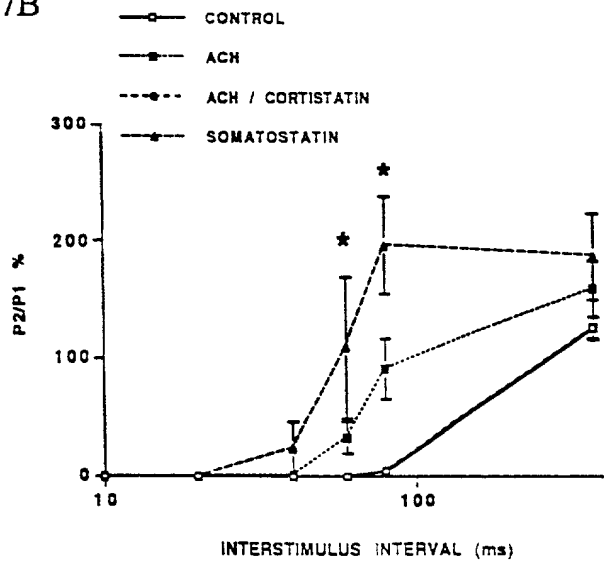


FIGURE 6

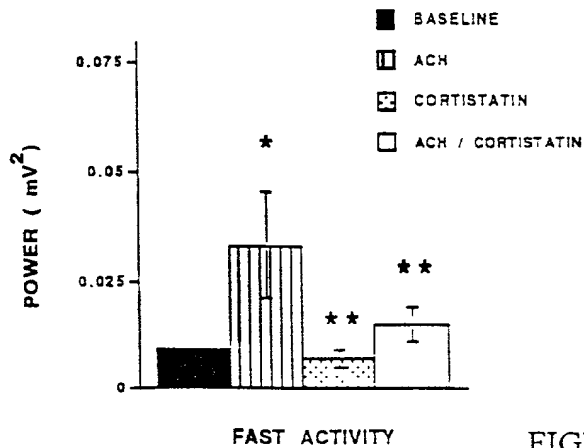
7A



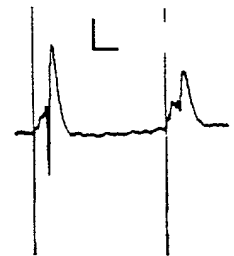
7B



7G



7C



7D



7E



7F

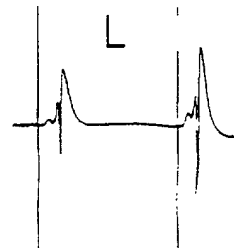


FIGURE 7